

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1.1	0.7	576	1	POLO_DROME	P53304 drosophila	
2	1.0	0.6	298	1	KPKS_HUMAN	P07557 homo sapien	
3	1.0	0.6	323	1	KRAF_MS36	P00532 murine sacculi	
4	1.0	0.6	328	1	RMIL_MOUSE	P28028 mus musculus	
5	1.0	0.6	367	1	RMIL_AVIL	P10533 avian retrovirus	
6	1.0	0.6	380	1	KMIL_AVIMH	P00531 avian retrovirus	
7	1.0	0.6	437	1	KRAA_MOUSE	P04627 mus musculus	
8	1.0	0.6	450	1	RMIL_AVEYL	P27966 avian retrovirus	
9	1.0	0.6	547	1	YMX1_CAEEL	P34509 caenorhabditis elegans	
10	1.0	0.6	603	1	PLKL_HUMAN	P53350 homo sapien	
11	1.0	0.6	603	1	PLKL_MOUSE	Q07832 mus musculus	
12	1.0	0.6	603	1	PLKL_RAT	Q62673 rattus norvegicus	
13	1.0	0.6	604	1	KRAA_RAT	P14056 rattus norvegicus	
14	1.0	0.6	606	1	KRAA_HUMAN	P10398 homo sapien	
15	1.0	0.6	606	1	KRAA_PIG	Q19004 sus scrofa	
16	1.0	0.6	638	1	KRAF_XENIA	P09560 xenopus laevis	
17	1.0	0.6	647	1	KMIL_CHICK	P05625 gallus gallus	
18	1.0	0.6	648	1	KRAF_HUMAN	P04049 homo sapien	
19	1.0	0.6	648	1	KRAF_RAT	P11365 rattus norvegicus	
20	1.0	0.6	765	1	KRAF_HUMAN	P15056 homo sapien	
21	1.0	0.6	781	1	KRAF_DROME	P11446 drosophila	
22	1.0	0.6	806	1	RMIL_CHICK	Q04982 gallus gallus	
23	1.0	0.6	807	1	RMIL_COQJA	P34308 coturnix coqui	
24	1.0	0.6	813	1	KRAF_CAEEL	P07792 caenorhabditis elegans	
25	9	0.5	294	1	NPM_CHICK	P16339 gallus gallus	
26	9	0.5	402	1	KRGS_AVISU	P00529 avian sarcoma	
27	9	0.5	507	1	KRGS_CHICK	P0841 gallus gallus	
28	9	0.5	515	1	KP68_MOUSE	Q01963 mus musculus	
29	9	0.5	607	1	YJK0_MOUSE	P43951 saccharomyces cerevisiae	
30	9	0.5	619	1	HRI_MOUSE	Q32299 mus musculus	
31	9	0.5	620	1	HRI_RAT	P05195 rattus norvegicus	
32	9	0.5	626	1	HRI_RABBIT	P33279 oryctolagus cuniculus	
33	9	0.5	683	1	PLOI_SCHPO	P50528 schizosaccharomyces pombe	

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: October 22, 2001, 01:27:29 ; Search time 17.02 Seconds
(without alignments)
3306.802 Million cell updates/sec

Title: US-09-515-806-2
Perfect score: 1613
Sequence: 1 MAGGRGAPGRDRPEPESYP.....YNIKVEKKVSVLFLYSYRDD 1643

Scoring table: OJIGO
Gappen 60.0 , Gapext. 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT	1	POLO_DROME	STANDARD;	PRT;	576 AA.
ID	POLO_DROME				
AC	P5304;				
DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DT	01-OCT-2000	(Rel. 40, Last annotation update)			
DE	PROTEIN KINASE POLO (EC 2.7.1. -).				
GN	POLO.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oxydendroidea; Drosophilidae; Drosophila.				
OX	NCBI-TAXID:7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CANTON-S.				
RX	MLIDLINE=92084000; PubMed=16608828;				
RA	Llamazares S., Moreira A., Tavares A., Girdham C., Spruce B.A., Gonzalez C., Kress R.E., Glover D.M., Sunkel C.E.;				
RA	"Polo" encodes a protein kinase homolog required for mitosis in Drosophila.				
RT	Genes Dev. 5:2153-2165(1991).				
RL	FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.				
CC	"Polo" encodes a protein kinase homolog required for mitosis in Drosophila.				
CC	"- SUBCELLULAR LOCATION: CYTOPLASMIC.				
CC	"- TISSUE SPECIFICITY: LARVAL DISCS, BRAIN AND TESTIS.				
CC	"- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
CC	CDC5/POLO SUBFAMILY.				
CC	-----				
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CC	-----				
DR	EMBL; X63361; CAA44963; 1; -				
DR	HSSP; P11362; 1EGI.				
DR	Flybase; FBgn003124; Polo.				
DR	InterPro; IPR007119; -.				
DR	InterPro; IPR00959; -.				
DR	InterPro; IPR00290; -.				
DR	Pfam; PF00659; Polo_box_2.				
DR	PFAM; PF00669; Pkinase_1.				
DR	PROSITE; PS00101; PROTEIN_KINASE_ATP; FALSE_NEG.				
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.				
DR	PROSITE; PS55011; PROTEIN_KINASE_DOM; 1.				
KW	Transferase; Serine/threonine-protein kinase; ATP-binding.				
FT	DOMAIN 25. 277 PROTEIN KINASE.				
FT	NP_BIND 31 39 ATP (BY SIMILARITY).				
FT	BINDING 54 54 BY SIMILARITY.				
FT	ACT_SITE 148 148 BY SIMILARITY.				
FT	DOMAIN 391 420 POLO-HOMOLOGY (PH2).				
SQ	SEQUENCE 576 AA; 66947 MW; B957BDA173FA57D3 CRC64;				

Query Match 0.7%; Score 11; DB 1; Length 576;
 Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; OC

QY 861 HVKIGDFGLAT 871
 Db 161 HVKIGDFGLAT 171

RESULT 2
 KPKS_HUMAN STANDARD:
 ID KPKS_HUMAN PRT; 298 AA.
 AC P07557; 07, Created
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-APR-1988 (Rel. 07, Last annotation update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PKS PROTO-ONCOGENE SERINE/TYROSINE-PROTEIN KINASE (EC 2.7.1.-)
 DE (CONCogene PKS1) (FRAGMENT).
 DE ARAF2 OR PKS OR PKSL.
 OS Homo sapiens (Human).
 OC Chordata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID:9606; [1]

CC SEQUENCE FROM N.A.
 RP PubMed:8613571;
 RX Shows T.W., Mountz J.D.;
 RA Mark G.E., Seeley T.W., Shows T.W., Mountz J.D.;
 RT *PKS, a raf-related sequence in humans;
 PC Natl. Acad. Sci. U.S.A. 83:6312-6316(1986).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC [1]

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 CC [1]

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 CC [1]

DR EMBL: M13829; AAB08754.1; -.
 DR PIR: A23341; TVHUPK.
 DR HSSP: P00523; 2PTK.
 DR InterPro: IPR000719; -.
 DR InterPro: IPR002290; -.
 DR Pfam: PF00069; kinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50012; Serine/threonine-protein kinase; proto-oncogene;
 KW ATP-binding.
 KW ATP-binding.
 FT NON_TER 1 1 PROTEIN KINASE.
 FT DOMAIN 19 279 PROTEIN KINASE.
 FT NP_BIND 25 33 ATP (BY SIMILARITY).
 FT BINDING 45 45 ATP (BY SIMILARITY).
 FT ACT_SITE 138 138 BY SIMILARITY.
 SQ SEQUENCE 298 AA; 33852 MW; 9AC38F65A7AAFFDD0 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 298;
 Best Local Similarity 100.0%; Pred. No. 0.099; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; OC

QY 862 VKIGDFGLAT 871
 Db 152 VKIGDFGLAT 161

RESULT 3
 KRAF_MSV36 STANDARD; PRT; 323 AA.
 AC P00332;

Query Match 0.6%; Score 10; DB 1; Length 323;
 Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; OC

QY 862 VKIGDFGLAT 871
 Db 157 VKIGDFGLAT 166

RESULT 4
 KRAF_MOUSE STANDARD; PRT; 328 AA.
 AC P28028;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE B-RAF PROTO-ONCOGENE SERINE/TYROSINE-PROTEIN KINASE (EC 2.7.1.-)
 DE (FRAGMENT).
 GN B-RAF OR B-RAF.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RN [1] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.; PubMed=2052597;
 RX MEDLINE=91271351; PubMed=2052597;
 RA Reynolds S.H., Aronson S.A., Molloy C.J., Blam S.B.,
 RA "Development of a highly efficient expression cDNA cloning system;
 RT application to oncogene isolation";
 RL Proc. Natl. Acad. Sci. U.S.A. 8:167-5171 (1991).
 CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS.
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF
 CC HIPPOCAMPAL NEURON.
 CC -1- DISEASE: PARTICIPATES IN A CHROMOSOMAL TRANSLLOCATION THAT PRODUCES
 CC A TIFLA-BRAF (T18) ONCOGENE ORIGINALLY ISOLATED FROM A FURFURAL-
 CC INDUCED HEPATOMA.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.

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 DR EMBL: M64429; AAA37320.1; ALT_INIT.
 DR PIR: A0951; TWSMBF.
 DR HSSP: P11362; IFGI.
 DR MGI: MGI:381190; Braf.
 DR InterPro: IPR00719; -.
 DR Pfam: PF00069; Pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; Proto-oncogene;
 KW ATP-Binding; Chromosomal translocation.
 FT DOMAIN 19 1 PROTEIN KINASE.
 FT DOMAIN 19 1 PROTEIN KINASE.
 FT NP_BIND 279 PROTEIN KINASE.
 FT BINDING 25 33 ATP (BY SIMILARITY).
 FT ACT_SITE 45 45 ATP (BY SIMILARITY).
 FT ACT_SITE 138 138 BY SIMILARITY.
 SQ SEQUENCE 328 AA: 36986 MW: 67A2BFB78A78E3D CRC64;

Query Match 0.68; Score 10; DB 1; Length 328;

Best Local Similarity 100.0%; Pred. No. 0 11;

Matches 10; Conservative 0; Mismatches 0; Gaps 0;

Indels 0; Standard; PRT; 367 AA.

QY 862 VKIGDFGLAT 871
 DB 152 VKIGDFGLAT 161

Query Match 0.68; Score 10; DB 1; Length 367;

Best Local Similarity 100.0%; Pred. No. 0 12;

Matches 10; Conservative 0; Mismatches 0; Gaps 0;

Indels 0; Standard; PRT; 380 AA.

QY 862 VKIGDFGLAT 871
 DB 200 VKIGDFGLAT 209

RESULT 6

RML_AVIMH

STANDARD

PRT;

380 AA.

V-MIL OR V-MHT.

Avian retroviruses

MH2.

Viruses

Retroviral

viruses

Retroviridae

Avian type C retroviruses.

OC Avian retrovirus IC10.

OC Viruses; Retroviral viruses

OC NCBI_TAXID=11874;

OC SEQUENCE FROM N.A.

OX NCBI_TAXID=11874;

OX SEQUENCE FROM N.A.

RX MEDLINE=89160254; PubMed=2537952;

RA Eychene A., Marx M., Dezelieu P., Calothy G.;

RT "Complete nucleotide sequence of IC10, a retrovirus containing the
 RT Rm1 oncogene transduced in chicken neuroretina cells infected with
 RT avian retrovirus RAV-1.";

RA Nucleic Acids Res. 17:1250(1989).

RN [2] SEQUENCE FROM N.A.

RX MEDLINE=89091077; PubMed=2851063;

RA Marx M., Eychene A., Laugier D., Bechade C., Crisanti P.,

RA Dezelieu P., Pessac B., Calothy G.;

RT "A novel oncogene related to c-mil is transduced in chicken

RT neuroretina cells induced to proliferate by infection with an avian

RT lymphomatosis virus.";

RA EMBO J. 7:3369-3373(1988).

CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-R-MIL

CC POLYPROTEIN.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC MIL/RAF SUBFAMILY.

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CC -1- DR EMBL: X13744; CAA32008.1; ALT_SEQ.

DR EMBL: X13438; CAA31790.1; ALT_SEQ.

DR PIR: S01645; TVFVAT.

DR HSSP: P11362; IFGI.

DR InterPro: IPR000719; -.

DR PIR: S01645; TVFVAT.

DR PROSITE: PS00069; Pkinase; 1.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

KW Polyprotein; Transforming protein; Serine/threonine-protein kinase;

KW Transferase; Oncogene; ATP-binding.

FT DOMAIN 67 327 PROTEIN KINASE.

FT NP_BIND 73 81 ATP (BY SIMILARITY).

FT BINDING 93 93 ATP (BY SIMILARITY).

FT ACT_SITE 186 186 BY SIMILARITY.

SQ SEQUENCE 367 AA: 41023 MW: E1374FCDCB9398A CRC64;

Query Match 0.68; Score 10; DB 1; Length 367;

Best Local Similarity 100.0%; Pred. No. 0 12;

Matches 10; Conservative 0; Mismatches 0; Gaps 0;

Indels 0; Standard; PRT; 380 AA.

QY 862 VKIGDFGLAT 871

DB 200 VKIGDFGLAT 209

RESULT 5

RML_AVIII

STANDARD

PRT;

380 AA.

V-MIL OR V-MHT.

Avian retroviruses

MH2.

Viruses

Retroviral

viruses

Retroviridae

Avian type C retroviruses.

OC Sequence FROM N.A.

RX MEDLINE=8191511; PubMed=6325930;

RA Sutrave P., Bonner T.I., Rapp U.R., Jansen H.W., Patschinsky T.,

RA	Bister K.; "Nucleotide sequence of avian retroviral oncogene v-mil: homologue of murine retroviral oncogene v-raf."; Nature 309:85-88(1984). [12]
RN	SEQUENCE FROM N.A.; MEDLINE=84121296; PubMed=6320371; RA Kan N.C.; Flordellis C.S.; Mark G.E.; Duesberg P.H.; Papas T.S.; RA "A common onc gene sequence transduced by avian carcinoma virus MH2 and by murine sarcoma virus 3611."; RT Science 222:813-816(1984). RT -!- DISEASE: BY ITSELF THE V-MIL ONCOGENE HAS ONLY WEAK TRANSFORMING CAPACITY BUT IT ABOLISHES THE GROWTH FACTOR REQUIREMENTS OF AVIAN MACROPHAGES TRANSFORMED BY OTHER ONCOGENES. RT -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-MHT OR GAG-MIL POLYPROTEIN. RT -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MIL/RAF SUBFAMILY. [1]
RR	----- CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
RX	----- CC EMBL; X00534; CAA25211.1; ALT_INIT. CC PIR; A00639; TVFYMM. CC HSSP; P11362; 1FG1. CC DR InterPro; IPRO00719; CC DR InterPro; IPRO02290; CC DR Pfam; PF0069; pkinase; 1. CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. CC DR PROSITE; PS00107; PROTEIN_KINASE_ST; 1. CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1. CC DR PROSITE; PS50011; PROTEIN_KINASE_DOR; 1. CC DR KW Polyprotein; Transforming protein; Serine/threonine-protein kinase; KW DOMAIN; 82 341 PROTEIN KINASE. FT DOMAIN FT NP_BIND 88 96 ATP (BY SIMILARITY). FT BINDING 108 108 ATP (BY SIMILARITY). FT ACT_SITE 201 201 BY SIMILARITY. FT CONFLICT 211 211 G -> E (IN REF. 2). SQ SEQUENCE 380 AA; 42853 MW; 6498695FB/EBEED CRC64;
RA	----- Query Match 0.6%; Score 10; DB 1; Length 380; Best Local Similarity 100.0%; Pred. No. 0.12; Mismatches 0; Indels 0; Gaps 0 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	862 VKIGDFGLAT 871
DB	215 VKIGDFGLAT 224
RESULT	7
RA	KRAA_MOUSE ID KRAA_MOUSE STANDARD; P04627; DT 13-AUG-1987 (Rel. 05, Created); DT 13-AUG-1987 (Rel. 05, Last sequence update); DT 01-OCT-2000 (Rel. 40, Last annotation update); DE A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) DE (FRAGMENT). DE ARAF1 OR ARAF OR A-RAF. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; OC Muridae; Murinae; Murinae; Murinae. OX NCBI_TAXID=10090; RN
RP	SEQUENCE FROM N.A. MEDLINE=8704566; PubMed=3491291; RX Colobochitidae M; Goldsbrough M; Cleveland J.; Gunnell M.; Bonner T.;

Rapp U.R.;
 "Characterization of murine A-raf, a new oncogene related to the
 v-raf oncogene";
 Mol. Cell. Biol. 6:2655-2662(1986).
 -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
 FROM THE CELL MEMBRANE TO THE NUCLEUS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
 MIL/RAF SUBFAMILY.
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 CC
 DR EMBL: D00024; BAA0018.1; -.
 DR P18: M13071; AAA37258.1; -.
 DR P18; A55382; TVMSRF.
 DR HSSP; P11362; 1FGI.
 DR MGD; MG1:88065; Araf.
 DR InterPro: IPR000719; -.
 DR InterPro: IPR002290; -.
 DR PROSITE: PS00069; pkinase; 1.
 DR PROSITE: PS000107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS000108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS500111; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; Proto-oncogene;
 ATP binding.
 KW
 FT DOMAIN 1 1 PROTEIN KINASE.
 FT 141 401 ATP (BY SIMILARITY).
 FT NP_BIND 147 155 ATP (BY SIMILARITY).
 FT BINDING 167 167 ATP (BY SIMILARITY).
 FT ACT_SITE 260 260 BY SIMILARITY.
 SQ SEQUENCE 437 AA; 487/92 MW; 1534011B018710ED CRC64;
 Query Match 0.6%; Score 10; DB 1; Length 437;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 SQ
 Qy 862 VKIGDFGLAT 871
 Db 2744 VKIGDFGLAT 283
 RESULT 8
 RMIL_AVEVR STANDARD; PRT; 450 AA.
 ID _RMIL_AVEVR
 AC P27966;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RMIL SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN
 DE (EC 2.7.1.-).
 DE V-RMIL.
 GN Avian rous-associated virus type 1.
 OC Viruses; Retroviruses; Retroviridae; Avian type C retrovirus
 OC NCBI_TAXID=11950;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91251215; PubMed=1645786;
 RA Felder M.P.; Eychenne A.; Barnier J.V.; Calogeraki I.; Calothy G
 RA Marx M.;
 RT "Common mechanism of retrovirus activation and transduction of
 RT and c-Rnili in chicken neuroretina cells infected with Rous-asso
 RT virus type 1.";
 RL J. Virol. 65:3633-3640(1991).
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A R-MIL-ENV
 CC POLYPROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
 CC MIL/RAF SUBFAMILY.

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EMBL; M62407; AAA2549.1; -
 PIR; A40341; TVFYNR.
 HSSP; P11362; 1FGI.
 DR InterPro; IPR00719; -
 DR InterPro; IPR002290; -
 Pfam; PF00069; pk kinase; 1.
 PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 Polyprotein; Transforming protein; Serine/threonine-protein kinase;
 Transfase; Oncogene; ATP-binding.
 DOMAIN 83 343 PROBIN KINASE.
 NP_BIND 89 97 ATP (BY SIMILARITY).
 BINDING 109 202 BY SIMILARITY.
 ACT_SITE 202 202 BY SIMILARITY.
 SEQUENCE 450 AA; 50313 MW; 6581AAF2253CB622 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 450;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 862 VKIGDFGLAT 871
 Db 216 VKIGDFGLAT 225

RESULT 9
 YMX1_CAEEL STANDARD; PRM; 547 AA.
 ID YMX1_CAEEL
 AC P34309;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PUTATIVE SERINE/THREONINE-PROTEIN KINASE K06H7.1 IN CHROMOSOME III
 DE (EC 2.7.1.-)
 GN K06H7.1
 OS Caenorhabditis elegans
 OC Eukaryota; Metazoa; Nematoidea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderaida; Caenorhabditis.
 NCBI_TaxID=6239;
 [1]
 RN SEQUENCE FROM N.A.
 STRAIN=BRISTOL N2;
 MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Croxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Jonson L., Jones M., Kershaw J., Kirsten J., Laisteller N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Shawken R.,
 RA Sims M., Smalldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaughn M., Vaughn K.,
 RA Waterson N., Watson A., Weinstock L., Wilkinsons-Sprout J.,
 RA Woldman P.;
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RRL Nature 368:32-38 (1994)
 CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
 CC PROTEIN KINASES.
 CC

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EMBL; L15314; AAA38084.1; -.

PIR; S44841; S44841.

DDR; HSSP; Q63450; 1A06.

WormPep; K06167.1; CE00252.

InterPro; IPR000719; -.

InterPro; IPR002290; -.

InterPro; IPR002291; -.

InterPro; IPR000659; kinase; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00118; PROTEIN_KINASE_ST; 1.

PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

Hypothetical protein; Transferase; Serine/threonine-protein kinase; ATP-binding.

KW DOMAIN 267 526 PROTEIN KINASE.

KW NP BIND 273 281 ATP (BY SIMILARITY).

KW FT BINDING 296 296 ATP (BY SIMILARITY).

KW ACT_SITE 390 390 BY SIMILARITY.

KW SEQUENCE 547 AA: 63490 MW: OOD28C2FFEAC63101 CRC64;

Query Match 0.68; Score 10; DB 1; Length 547;

Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 10; conservative 0; Mismatches 0; Indels 0; caps 0;

Dy 862 VKIGDFGLAT 871

Db 404 VKIGDFGLAT 413

RESULT 10

PK1_HUMAN

PUR1_HUMAN

STANDARD:

PRIT:

603 AA.

AC P53350;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE SERINE/THREONINE-PROTEIN KINASE PLK (EC 2.7.1.-) (PLK-1) (SERINE-THREONINE PROTEIN KINASE 13) (STPK13).

DE PLK OR PLK1.

EN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]

RN SEQUENCE FROM N.A.

RP TISSUE=Placenta;

RC MEDLINE=942489293; PubMed=8018557;

RA Hamanaka R., Maloof S., Smith M.R., O'Connell C.D., Longo D.L., Ferris D.K.;

RA "Cloning and characterization of human and murine homologues of the Drosophila polo serine-threonine kinase.";

RT Cell Growth Differ. 5:249-257(1994).

[2]

RN SEQUENCE FROM N.A.

RP MEDLINE=94067140; PubMed=7902533;

RA Lake R.J., Jelinek W.R.;

RT "Cell cycle- and terminal differentiation-associated regulation of the mouse mRNA encoding a conserved mitotic protein kinase.";

RT Mol. Cell. Biol. 13:7793-7801(1993).

[3]

RN SEQUENCE FROM N.A.

RP MEDLINE=95051109; PubMed=7962193;

RA Colsteyn R.M., Schultz S.J., Bartek J., Ziemiczki A., Ried T., Nigg E.A.;

RA "Cell cycle analysis and chromosomal localization of human Plk1, a putative homologue of the mitotic kinases drosophila polo and Saccharomyces cerevisiae Cdc5.";

RT J. Cell. Sci. 107 Pt 1:1509-1517(1994).

RT 3L

FT	NP_BIND	314	322	ATP (BY SIMILARITY).	DR	PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
FT	BINDING	334	334	ATP (BY SIMILARITY).	DR	PROSITE; PS500107; PROTEIN_KINASE_ATP; 1.
FT	ACT_SITE	427	427	BY SIMILARITY.	DR	PROSITE; PS500111; PROTEIN_KINASE_ATP; 1.
SQ	SEQUENCE	604 AA;	67551 MW;	FF24FB2170B0B115 CRC64;	DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Query Match		0.68;	Score 10;	DB 1;	KW	Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
Best Local Similarity		100.08;	Pred. No. 0.18;	Length 604;	FT	ATP-binding; Phorbol-ester and DAG BINDING.
Matches 10;	Conservative	0;	Mismatches 0;	Indels 0;	FT	PROTEIN_KINASE;
01-MAR-1989 (Rel. 10, Created)					FT	Protein kinase;
01-OCT-1996 (Rel. 34, Last sequence update)					FT	Phorbol-ester binding.
01-OCT-2000 (Rel. 40, Last annotation update)					FT	Protein kinase;
DE-ARAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-)					FT	Phorbol-ester and DAG BINDING.
DE (ONCOGENE PKS2).					FT	Protein kinase;
OS	Homo sapiens (Human).				FT	Phorbol-ester and DAG BINDING.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				FT	Protein kinase;
OC	Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.				FT	Phorbol-ester and DAG BINDING.
NCBI_TaxID=9606;					FT	Protein kinase;
[1]					FT	Phorbol-ester and DAG BINDING.
SEQUENCE FROM N.A.					FT	Protein kinase;
MEDLINE-87146380; PubMed=3029685;					FT	Phorbol-ester and DAG BINDING.
RX	Beck T.W., Huleihel M., Gurnell M., Bonner T.I., Rapp U.R.;				FT	Protein kinase;
RA	"The complete coding sequence of the human A-raf-1 oncogene and				FT	Phorbol-ester and DAG BINDING.
RA	transforming activity of a human A-raf carrying retrovirus."				FT	Protein kinase;
RT	Nucleic Acids Res. 15:595-609(1987).				FT	Phorbol-ester and DAG BINDING.
RN	SEQUENCE FROM N.A.				FT	Protein kinase;
RC	TISSUE=Placenta;				FT	Phorbol-ester and DAG BINDING.
RX	Lee J.E., Beck T.W., Brennscheidt U., Degennaro L.J., Rapp U.R.;				FT	Protein kinase;
RT	"The complete sequence and promoter activity of the human A-raf-1 gene (ARAF1)." ;				FT	Phorbol-ester and DAG BINDING.
RL	Genomics 20:43-55(1994).				FT	Protein kinase;
CC	-!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS				FT	Phorbol-ester and DAG BINDING.
CC	FROM THE CELL MEMBRANE TO THE NUCLEUS.				FT	Protein kinase;
CC	-!- TISSUE SPECIFICITY: PREDOMINANTLY IN UROGENITAL TISSUES (BY SIMILARITY).				FT	Phorbol-ester and DAG BINDING.
CC	-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				FT	Protein kinase;
CC	MIL/RAF SUBFAMILY.				FT	Phorbol-ester and DAG BINDING.
CC	-!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.				FT	Protein kinase;
CC	EMBL: L24038; AAA65219.1; -.				FT	Phorbol-ester and DAG BINDING.
CC	DR	EMBL: U01337; ARB03517.1; -.			FT	Phorbol-ester and DAG BINDING.
CC	DR	PIR: A26439; TVHDAP.			FT	Phorbol-ester and DAG BINDING.
CC	DR	HSSP: P04049; IFAQ.			FT	Phorbol-ester and DAG BINDING.
CC	DR	MIM: 311010; -.			FT	Phorbol-ester and DAG BINDING.
CC	DR	InterPro: IPR000719; -.			FT	Phorbol-ester and DAG BINDING.
CC	DR	InterPro: IPR002230; -.			FT	Phorbol-ester and DAG BINDING.
CC	DR	Pfam: PF00069; pk kinase.			FT	Phorbol-ester and DAG BINDING.
CC	DR	PRINTS: PRO0009; DAGPEOMAIN.			FT	Phorbol-ester and DAG BINDING.
CC	DR	PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.			FT	Phorbol-ester and DAG BINDING.
CC	DR	PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.			FT	Phorbol-ester and DAG BINDING.
CC	DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			FT	Phorbol-ester and DAG BINDING.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 RW Transerase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
 ATP-binding; Phorbol-ester binding.
 FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.
 FT DOMAIN 310 570 PROTEIN_KINASE.
 FT NP_BIND 316 324 ATP (BY SIMILARITY).
 FT BINDING 336 336 ATP (BY SIMILARITY).
 FT ACT_SITE 429 429 BY SIMILARITY.
 FT SEQUENCE 606 AA; 67538 MW; 1A7EEB9A5D9DE152 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 606;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 862 VKIGDFGLAT 871
 Db 443 VKIGDFGLAT 452

Search completed: October 22, 2001, 01:31:53
 Job time: 264 sec

